


GROSE et al.
Serial No. 09/646,224

the errors noted in the Raw Sequence Listing Error Report which was attached to the Office communication of October 23, 2001 (copy attached). The Office is requested to contact the undersigned if anything further is required in this regard.

An early and favorable Action on the merits is requested.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: 

B. J. Sadoff
Reg. No. 36,663

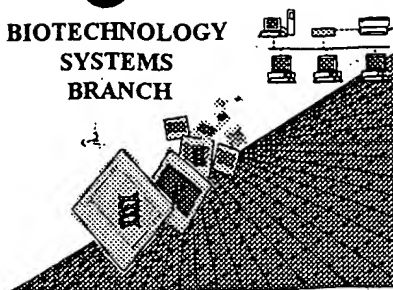
BJS:eaw
1100 North Glebe Road, 8th Floor
Arlington, VA 22201-4714
Telephone: (703) 816-4000
Facsimile: (703) 816-4100

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NOV 02 2001

TECH CENTER 1600/2900

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

APPLICANT COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/646,224

Source: OIPe

Date Processed by STIC: 9/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/646,224

DATE: 09/18/2001

TIME: 10:11:16

Input Set : A:\Pg3432.app

Output Set: N:\CRF3\09182001\I646224.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Glaxo Wellcome PLC
5 Tate, Simon N
6 Grose, David T
7 Hicks, Caroline A
9 <120> TITLE OF INVENTION: Ion Channels
11 <130> FILE REFERENCE: PG3432
13 <140> CURRENT APPLICATION NUMBER: US/09/646,224
14 <141> CURRENT FILING DATE: 2001-08-30
16 <150> PRIOR APPLICATION NUMBER: GB 9805793.8
17 <151> PRIOR FILING DATE: 1998-03-18
19 <160> NUMBER OF SEQ ID NOS: 35
21 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

500 <210> SEQ ID NO: 2
501 <211> LENGTH: 1765
502 <212> TYPE: PRT
503 <213> ORGANISM: Rattus norvegicus
505 <400> SEQUENCE: 2
506 Met Glu Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe
507 1 5 10 15
509 Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala
510 20 25 30
512 Ile Gln Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro
513 35 40 45
515 Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys
516 50 55 60
518 Leu Tyr Gly Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp
519 65 70 75 80
521 Leu Asp Pro Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys
522 85 90 95
524 Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu
525 100 105 110
527 Gly Pro Phe Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His
528 115 120 125
530 Ser Val Phe Ser Met Phe Ile Cys Thr Val Ile Ile Asn Cys Met
531 130 135 140
533 Phe Met Ala Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu
534 145 150 155 160
536 Tyr Val Phe Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu
537 165 170 175
539 Ala Arg Gly Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp
540 180 185 190
542 Asn Trp Leu Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe
543 195 200 205

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Input Set : A:\Pg3432.app

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545 Pro Gly Ser Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe
546      210                      215                      220
548 Arg Ala Leu Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val
549 225                      230                      235                      240
551 Gly Ala Leu Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu
552                      245                      250                      255
554 Thr Leu Phe Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe
555                      260                      265                      270
557 Met Gly Ile Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn
558                      275                      280                      285
560 Pro Ala Ser Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp
561                      290                      295                      300
563 Phe Ile Met Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly
564 305                      310                      315                      320
566 Ser Thr Cys Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys
567                      325                      330                      335
569 Phe Asp Asn Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr
570                      340                      345                      350
572 Gln Asp Ser Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly
573                      355                      360                      365
575 Ile Tyr Phe Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe
576                      370                      375                      380
578 Tyr Leu Leu Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu
579 385                      390                      395                      400
581 Gln Asn Arg Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe
582                      405                      410                      415
584 Gln Glu Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala
585                      420                      425                      430
587 Met Gly Ile Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe
588                      435                      440                      445
590 Ser Pro Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe
591                      450                      455                      460
593 Phe Met Arg Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu
594 465                      470                      475                      480
596 Asp Asp Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu
597                      485                      490                      495
599 Ser Gln Asn Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu
600                      500                      505                      510
602 His Arg Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile
603                      515                      520                      525
605 Gln Glu Gln Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn
606                      530                      535                      540
608 Leu Ala Ser Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys
609 545                      550                      555                      560
611 Ile Lys Lys Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu
612                      565                      570                      575
614 Ala Ile Thr Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu
615                      580                      585                      590
617 His His Asn Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn

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618	595	600	605
620 Trp Val Phe Thr Gly Ile	Phe Ile Ala Glu Met Cys Leu Lys Ile Ile		
621 610	615	620	
623 Ala Leu Asp Pro Tyr His	Tyr Phe Arg His Gly Trp Asn Val Phe Asp		
624 625	630	635	640
626 Ser Ile Val Ala Leu Ser	Leu Ala Asp Val Leu Tyr Asn Thr Leu		
627	645	650	655
629 Ser Asp Asn Asn Arg Ser	Phe Leu Ala Ser Leu Arg Val Leu Arg Val		
630	660	665	670
632 Phe Lys Leu Ala Lys Ser	Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile		
633	675	680	685
635 Ile Gly His Ser Val Gly	Ala Leu Gly Asn Leu Thr Val Val Leu Thr		
636 690	695	700	
638 Ile Val Val Phe Ile Phe	Ser Val Val Gly Met Arg Leu Phe Gly Thr		
639 705	710	715	720
641 Lys Phe Asn Lys Thr Ala	Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg		
642	725	730	735
644 Trp His Met Asp Asn Phe	Tyr His Ser Phe Leu Val Val Phe Arg Ile		
645	740	745	750
647 Leu Cys Gly Glu Trp Ile	Glu Asn Met Trp Gly Cys Met Gln Asp Met		
648	755	760	765
650 Asp Gly Ser Pro Leu Cys	Ile Ile Val Phe Val Leu Ile Met Val Ile		
651 770	775	780	
653 Gly Lys Leu Val Val Leu	Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser		
654 785	790	795	800
656 Phe Ser Asn Glu Glu Lys	Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys		
657	805	810	815
659 Thr Lys Val Gln Leu Ala	Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe		
660	820	825	830
662 Met Leu His Ala Leu Gln	Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys		
663	835	840	845
665 Asn Ser Pro Lys Pro Lys	Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn		
666 850	855	860	
668 Lys Asp Ser Ile Leu Pro	Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr		
669 865	870	875	880
671 Asp Met Ala Leu Tyr Thr	Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu		
672	885	890	895
674 Ala Glu Val Glu Asp Asp	Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu		
675	900	905	910
677 Pro Thr Ser Gln His Ser	Ala Gly Val Gln Ala Gly Asp Leu Pro Pro		
678	915	920	925
680 Glu Thr Lys Gln Leu Thr	Ser Pro Asp Asp Gln Gly Val Glu Met Glu		
681 930	935	940	
683 Val Phe Ser Glu Glu Asp	Leu His Leu Ser Ile Gln Ser Pro Arg Lys		
684 945	950	955	960
686 Lys Ser Asp Ala Val Ser	Met Leu Ser Glu Cys Ser Thr Ile Asp Leu		
687	965	970	975
689 Asn Asp Ile Phe Arg Asn	Leu Gln Lys Thr Val Ser Pro Lys Lys Gln		
690	980	985	990

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```

692 Pro Asp Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His
693          995          1000          1005
695 Lys Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg
696    1010          1015          1020
698 Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile
E--> 699 025 1005          1030          1035          1040
701 Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val
702          1045          1050          1055
704 Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp
705          1060          1065          1070
707 Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val
708    1075          1080          1085
710 Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp
711    1090          1095          1100
713 Phe Leu Ile Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser
E--> 714 105 1105          1110          1115          1120
716 Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu
717          1125          1130          1135
719 Ser Gln Phe Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala
720          1140          1145          1150
722 Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu
723          1155          1160          1165
725 Val Phe Cys Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg
726    1170          1175          1180
728 Cys Ile Asn Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val
E--> 729 185 1185          1190          1195          1200
731 Pro Asn Arg Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro
732          1205          1210          1215
734 Gln Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln
735          1220          1225          1230
737 Val Ala Thr Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp
738    1235          1240          1245
740 Ser Arg Glu Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala
741    1250          1255          1260
743 Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu
E--> 744 265 1265          1270          1275          1280
746 Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys
747          1285          1290          1295
749 Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr
750          1300          1305          1310
752 Tyr Asn Ala Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile
753          1315          1320          1325
755 Pro Arg Pro Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr
756    1330          1335          1340
758 Ser Gln Val Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met
E--> 759 345 1345          1350          1355          1360
761 Ile Ile Met Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys
762          1365          1370          1375
764 Thr Phe Asp Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu

```

When
numbering
first amino
acid on a
line, begin
number directly
under first
letter of amino
acid

e.g. Lys
1025

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```

765          1380          1385          1390
767 Cys Leu Ile Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly
768          1395          1400          1405
770 Trp Asn Leu Phe Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr
771          1410          1415          1420
773 Leu Val Ser Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu
E--> 774 425          1430          1435          1440
776 Phe Arg Val Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val
777          1445          1450          1455
779 Arg Ala Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser
780          1460          1465          1470
782 Leu Pro Ser Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe
783          1475          1480          1485
785 Ile Tyr Ala Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly
786          1490          1495          1500
788 Ser Gly Ile Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met
E--> 789 505          1510          1515          1520
791 Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu
792          1525          1530          1535
794 Asn Pro Met Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp
795          1540          1545          1550
797 Ser Cys Gln Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile
798          1555          1560          1565
800 Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
801          1570          1575          1580
803 Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu
E--> 804 585          1590          1595          1600
806 Asp Asp Phe Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu
807          1605          1610          1615
809 Ala Ser Gln Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala
810          1620          1625          1630
812 Leu Pro Glu Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu
813          1635          1640          1645
815 Val Met Asp Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp
816          1650          1655          1660
818 Val Leu Phe Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu
E--> 819 665          1670          1675          1680
821 Asp Thr Met Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro
822          1685          1690          1695
824 Phe Lys Lys Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu
825          1700          1705          1710
827 Glu Glu Gln Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met
828          1715          1720          1725
830 Glu Lys Met Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser Ser His
831          1730          1735          1740
833 Glu Val Phe Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val
E--> 834 745          1750          1755          1760
836 Lys Val His Asn Asp
837          1765

```

*same
even*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/646,224

DATE: 09/18/2001

TIME: 10:11:17

Input Set : A:\Pg3432.app

Output Set: N:\CRF3\09182001\I646224.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:699 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2